



W661: Could Small Seeded Wild Relatives of Cultivated Peanut be used to Increase the Size of Peanut Seeds?

Saturday, January 13, 2018

09:20 AM - 09:40 AM

📍 *Royal Palm Salon 5-6*

Seed size is a major agronomic trait that has been selected in crops during the domestication process. However, many studies reported agronomically important alleles that have been left behind or lost during this process. Cultivated peanut is characterized by the paucity of DNA polymorphism. Conversely, high level of polymorphism exists with peanut wild relatives that can be harnessed together with important agronomic traits to improve the cultivated varieties. In a collaborative project with CIRAD, ISRA, UGA and EMBRAPA we developed interspecific QTL mapping populations (AB-QTL and CSSL) for identifying and tracing back the favorable wild alleles in breeding programs. We identified several genomic regions associated with seed size increase in two AB-QTL populations that shared a common recurrent parent. A CSSL population developed from the cross between Fleur11 and (*A. ipaensis* x *A. duranensis*)^{4x} was used to validate those QTLs. The CSSL population is of particular interest as it represents the entire wild species genomes in a set of lines each carrying one or a few wild donor segments in the genetic background of the cultivated peanut. This allows mendelizing the QTLs, which ease their used in breeding programs. Several CSSLs that carry wild chromosome segments involved in seed size increase were crossed for pyramiding the QTLs. Additive effects were observed indicating that pyramiding of wild alleles has significant potential for increasing seed size in peanut. The recent release of the peanut genomes opens new avenues for understanding the genomic mechanisms that favored the lost of benefic alleles in cultivated peanut.

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